

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/041,236

INPUT SET: S30140.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4 (i) APPLICANT: Luo, Yuling  
5 Xiomei, Xu  
6 (ii) TITLE OF INVENTION: Semaphorin K1  
7 (iii) NUMBER OF SEQUENCES: 4  
8 (iv) CORRESPONDENCE ADDRESS:  
9 (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
10 (B) STREET: 75 DENISE DRIVE  
11 (C) CITY: HILLSBOROUGH  
12 (D) STATE: CALIFORNIA  
13 (E) COUNTRY: USA  
14 (F) ZIP: 94010  
15 (v) COMPUTER READABLE FORM:  
16 (A) MEDIUM TYPE: Floppy disk  
17 (B) COMPUTER: IBM PC compatible  
18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
20 (vi) CURRENT APPLICATION DATA:  
21 (A) APPLICATION NUMBER: 09/041,236  
22 (B) FILING DATE: March 11, 1998  
23 (C) CLASSIFICATION:  
24 (viii) ATTORNEY/AGENT INFORMATION:  
25 (A) NAME: OSMAN, RICHARD A  
26 (B) REGISTRATION NUMBER: 36,627  
27 (C) REFERENCE/DOCKET NUMBER: EXEL98-001  
28 (ix) TELECOMMUNICATION INFORMATION:  
29 (A) TELEPHONE: (650) 343-4341  
30 (B) TELEFAX: (650) 343-4342  
31  
32 (2) INFORMATION FOR SEQ ID NO:1:  
33 (i) SEQUENCE CHARACTERISTICS:  
34 (A) LENGTH: 2498 base pairs  
35 (B) TYPE: nucleic acid  
36 (C) STRANDEDNESS: double  
37 (D) TOPOLOGY: linear  
38 (ii) MOLECULE TYPE: cDNA  
39 (ix) FEATURE:  
40 (A) NAME/KEY: CDS  
41 (B) LOCATION: 1..1902  
42 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
43 CTG CTG CTG CTG CTC TGG GCG GCC GCC GCC TCC GCC CAG GGC CAC CTA 48  
44 Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu  
45 1 5 10 15  
46 AGG AGC GGA CCC CGC ATC TTC GCC GTC TGG AAA GGC CAT GTA GGG CAG 96

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/041,236

DATE: 12/03/98  
TIME: 13:51:20

INPUT SET: S30140.raw

47	Arg	Ser	Gly	Pro	Arg	Ile	Phe	Ala	Val	Trp	Lys	Gly	His	Val	Gly	Gln	
48				20					25					30			
49	GAC	CGG	GTG	GAC	TTT	GGC	CAG	ACT	GAG	CCG	CAC	ACG	GTG	CTT	TTC	CAC	144
50	Asp	Arg	Val	Asp	Phe	Gly	Gln	Thr	Glu	Pro	His	Thr	Val	Leu	Phe	His	
51			35					40					45				
52	GAG	CCA	GGC	AGC	TCC	TCT	GTG	TGG	GTG	GGA	GGA	CGT	GGC	AAG	GTC	TAC	192
53	Glu	Pro	Gly	Ser	Ser	Ser	Val	Trp	Val	Gly	Gly	Arg	Gly	Lys	Val	Tyr	
54			50				55					60					
55	CTC	TTT	GAC	TTC	CCC	GAG	GGC	AAG	AAC	GCA	TCT	GTG	CGC	ACG	GTG	AAT	240
56	Leu	Phe	Asp	Phe	Pro	Glu	Gly	Lys	Asn	Ala	Ser	Val	Arg	Thr	Val	Asn	
57			65			70					75				80		
58	ATC	GGC	TCC	ACA	AAG	GGG	TCC	TGT	CTG	GAT	AAG	CGG	GAC	TGC	GAG	AAC	288
59	Ile	Gly	Ser	Thr	Lys	Gly	Ser	Cys	Leu	Asp	Lys	Arg	Asp	Cys	Glu	Asn	
60					85				90						95		
61	TAC	ATC	ACT	CTC	CTG	GAG	AGG	CGG	AGT	GAG	GGG	CTG	CTG	GCC	TGT	GGC	336
62	Tyr	Ile	Thr	Leu	Leu	Glu	Arg	Arg	Ser	Glu	Gly	Leu	Leu	Ala	Cys	Gly	
63				100					105					110			
64	ACC	AAC	GCC	CGG	CAC	CCC	AGC	TGC	TGG	AAC	CTG	GTG	AAT	GGC	ACT	GTG	384
65	Thr	Asn	Ala	Arg	His	Pro	Ser	Cys	Trp	Asn	Leu	Val	Asn	Gly	Thr	Val	
66			115					120					125				
67	GTG	CCA	CTT	GGC	GAG	ATG	AGA	GGC	TAC	GCC	CCC	TTC	AGC	CCG	GAC	GAG	432
68	Val	Pro	Leu	Gly	Glu	Met	Arg	Gly	Tyr	Ala	Pro	Phe	Ser	Pro	Asp	Glu	
69			130				135					140					
70	AAC	TCC	CTG	GTT	CTG	TTT	GAA	GGG	GAC	GAG	GTG	TAT	TCC	ACC	ATC	CGG	480
71	Asn	Ser	Leu	Val	Leu	Phe	Glu	Gly	Asp	Glu	Val	Tyr	Ser	Thr	Ile	Arg	
72			145			150					155					160	
73	AAG	CAG	GAA	TAC	AAT	GGG	AAG	ATC	CCT	CGG	TTC	CGC	CGC	ATC	CGG	GGC	528
74	Lys	Gln	Glu	Tyr	Asn	Gly	Lys	Ile	Pro	Arg	Phe	Arg	Arg	Ile	Arg	Gly	
75					165				170					175			
76	GAG	AGT	GAG	CTG	TAC	ACC	AGT	GAT	ACT	GTC	ATG	CAG	AAC	CCA	CAG	TTC	576
77	Glu	Ser	Glu	Leu	Tyr	Thr	Ser	Asp	Thr	Val	Met	Gln	Asn	Pro	Gln	Phe	
78				180					185					190			
79	ATC	AAA	GCC	ACC	ATC	GTG	CAC	CAA	GAC	CAG	GCT	TAC	GAT	GAC	AAG	ATC	624
80	Ile	Lys	Ala	Thr	Ile	Val	His	Gln	Asp	Gln	Ala	Tyr	Asp	Asp	Lys	Ile	
81			195					200					205				
82	TAC	TAC	TTC	TTC	CGA	GAG	GAC	AAT	CCT	GAC	AAG	AAT	CCT	GAG	GCT	CCT	672
83	Tyr	Tyr	Phe	Phe	Arg	Glu	Asp	Asn	Pro	Asp	Lys	Asn	Pro	Glu	Ala	Pro	
84			210				215					220					
85	CTC	AAT	GTG	TCC	CGT	GTG	GCC	CAG	TTG	TGC	AGG	GGG	GAC	CAG	GGT	GGG	720
86	Leu	Asn	Val	Ser	Arg	Val	Ala	Gln	Leu	Cys	Arg	Gly	Asp	Gln	Gly	Gly	
87			225			230					235				240		
88	GAA	AGT	TCA	CTG	TCA	GTC	TCC	AAG	TGG	AAC	ACT	TTT	CTG	AAA	GCC	ATG	768
89	Glu	Ser	Ser	Leu	Ser	Val	Ser	Lys	Trp	Asn	Thr	Phe	Leu	Lys	Ala	Met	
90				245					250					255			
91	CTG	GTA	TGC	AGT	GAT	GCT	GCC	ACC	AAC	AAG	AAC	TTC	AAC	AGG	CTG	CAA	816
92	Leu	Val	Cys	Ser	Asp	Ala	Ala	Thr	Asn	Lys	Asn	Phe	Asn	Arg	Leu	Gln	
93			260					265					270				
94	GAC	GTC	TTC	CTG	CTC	CCT	GAC	CCC	AGC	GGC	CAG	TGG	AGG	GAC	ACC	AGG	864
95	Asp	Val	Phe	Leu	Leu	Pro	Asp	Pro	Ser	Gly	Gln	Trp	Arg	Asp	Thr	Arg	
96			275					280					285				
97	GTC	TAT	GGT	GTT	TTC	TCC	AAC	CCC	TGG	AAC	TAC	TCA	GCC	GTC	TGT	GTG	912
98	Val	Tyr	Gly	Val	Phe	Ser	Asn	Pro	Trp	Asn	Tyr	Ser	Ala	Val	Cys	Val	
99			290				295					300					

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/041,236

DATE: 12/03/98  
TIME: 13:51:21

INPUT SET: S30140.raw

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101	Tyr	Ser	Leu	Gly	Asp	Ile	Asp	Lys	Val	Phe	Arg	Thr	Ser	Ser	Leu	Lys	
102	305				310						315					320	
103	GGC	TAC	CAC	TCA	AGC	CTT	CCC	AAC	CCG	CGG	CCT	GGC	AAG	TGC	CTC	CCA	1008
104	Gly	Tyr	His	Ser	Ser	Leu	Pro	Asn	Pro	Arg	Pro	Gly	Lys	Cys	Leu	Pro	
105				325						330						335	
106	GAC	CAG	CAG	CCG	ATA	CCC	ACA	GAG	ACC	TTC	CAG	GTG	GCT	GAC	CGT	CAC	1056
107	Asp	Gln	Gln	Pro	Ile	Pro	Thr	Glu	Thr	Phe	Gln	Val	Ala	Asp	Arg	His	
108				340						345						350	
109	CCA	GAG	GTG	GCG	CAG	AGG	GTG	GAG	CCC	ATG	GGG	CCT	CTG	AAG	ACG	CCA	1104
110	Pro	Glu	Val	Ala	Gln	Arg	Val	Glu	Pro	Met	Gly	Pro	Leu	Lys	Thr	Pro	
111			355						360							365	
112	TTG	TTC	CAC	TCT	AAA	TAC	CAC	TAC	CAG	AAA	GTG	GCC	GTC	CAC	CGC	ATG	1152
113	Leu	Phe	His	Ser	Lys	Tyr	His	Tyr	Gln	Lys	Val	Ala	Val	His	Arg	Met	
114	370						375						380				
115	CAA	GCC	AGC	CAC	GGG	GAG	ACC	TTT	CAT	GTG	CTT	TAC	CTA	ACT	ACA	GAC	1200
116	Gln	Ala	Ser	His	Gly	Glu	Thr	Phe	His	Val	Leu	Tyr	Leu	Thr	Thr	Asp	
117	385				390						395					400	
118	AGG	GGC	ACT	ATC	CAC	AAG	GTG	GTG	GAA	CCG	GGG	GAG	CAG	GAG	CAC	AGC	1248
119	Arg	Gly	Thr	Ile	His	Lys	Val	Val	Glu	Pro	Gly	Glu	Gln	Glu	His	Ser	
120				405						410						415	
121	TTC	GCC	TTC	AAC	ATC	ATG	GAG	ATC	CAG	CCC	TTC	CGC	CGC	GCG	GCT	GCC	1296
122	Phe	Ala	Phe	Asn	Ile	Met	Glu	Ile	Gln	Pro	Phe	Arg	Arg	Ala	Ala	Ala	
123			420						425						430		
124	ATC	CAG	ACC	ATG	TCG	CTG	GAT	GCT	GAG	CGG	AGG	AAG	CTG	TAT	GTG	AGC	1344
125	Ile	Gln	Thr	Met	Ser	Leu	Asp	Ala	Glu	Arg	Arg	Lys	Leu	Tyr	Val	Ser	
126			435					440					445				
127	TCC	CAG	TGG	GAG	GTG	AGC	CAG	GTG	CCC	CTG	GAC	CTG	TGT	GAG	GTC	TAT	1392
128	Ser	Gln	Trp	Glu	Val	Ser	Gln	Val	Pro	Leu	Asp	Leu	Cys	Glu	Val	Tyr	
129		450				455						460					
130	GGC	GGG	GGC	TGC	CAC	GGT	TGC	CTC	ATG	TCC	CGA	GAC	CCC	TAC	TGC	GGC	1440
131	Gly	Gly	Gly	Cys	His	Gly	Cys	Leu	Met	Ser	Arg	Asp	Pro	Tyr	Cys	Gly	
132	465				470						475					480	
133	TGG	GAC	CAA	GGC	CGC	TGC	ATC	TCC	ATC	TAC	AGC	TCC	GAA	CGG	TCA	GTG	1488
134	Trp	Asp	Gln	Gly	Arg	Cys	Ile	Ser	Ile	Tyr	Ser	Ser	Glu	Arg	Ser	Val	
135			485						490						495		
136	CTG	CAA	TCC	ATT	AAT	CCA	GCC	GAG	CCA	CAC	AAG	GAG	TGT	CCC	AAC	CCC	1536
137	Leu	Gln	Ser	Ile	Asn	Pro	Ala	Glu	Pro	His	Lys	Glu	Cys	Pro	Asn	Pro	
138			500						505						510		
139	AAA	CCA	GAC	AAG	GCC	CCA	CTG	CAG	AAG	GTT	TCC	CTG	GCC	CCA	AAC	TCT	1584
140	Lys	Pro	Asp	Lys	Ala	Pro	Leu	Gln	Lys	Val	Ser	Leu	Ala	Pro	Asn	Ser	
141			515						520						525		
142	CGC	TAC	TAC	CTG	AGC	TGC	CCC	ATG	GAA	TCC	CGC	CAC	GCC	ACC	TAC	TCA	1632
143	Arg	Tyr	Tyr	Leu	Ser	Cys	Pro	Met	Glu	Ser	Arg	His	Ala	Thr	Tyr	Ser	
144		530					535					540					
145	TGG	CGC	CAC	AAG	GAG	AAC	GTG	GAG	CAG	AGC	TGC	GAA	CCT	GGT	CAC	CAG	1680
146	Trp	Arg	His	Lys	Glu	Asn	Val	Glu	Gln	Ser	Cys	Glu	Pro	Gly	His	Gln	
147	545				550						555					560	
148	AGC	CCC	AAC	TGC	ATC	CTG	TTC	ATC	GAG	AAC	CTC	ACG	GCG	CAG	CAG	TAC	1728
149	Ser	Pro	Asn	Cys	Ile	Leu	Phe	Ile	Glu	Asn	Leu	Thr	Ala	Gln	Gln	Tyr	
150				565						570						575	
151	GGC	CAC	TAC	TTC	TGC	GAG	GCC	CAG	GAG	GGC	TCC	TAC	TTC	CGC	GAG	GCT	1776
152	Gly	His	Tyr	Phe	Cys	Glu	Ala	Gln	Glu	Gly	Ser	Tyr	Phe	Arg	Glu	Ala	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/041,236

DATE: 12/03/98  
TIME: 13:51:23

INPUT SET: S30140.raw

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153          580          585          590
154 CAG CAC TGG CAG CTG CTG CCC GAG GGC ATC ATG GCC GAG CAC CTG      1824
155 Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu
156          595          600          605
157 CTG GGT CAT GCC TGT GCC CTG GCC GCC TCC CTC TGG CTG GGG GTG CTG      1872
158 Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu
159          610          615          620
160 CCC ACA CTC ACT CTT GGC TTG CTG GTC CAC TAGGGCCTCC CGAGGCTGGG      1922
161 Pro Thr Leu Thr Leu Gly Leu Leu Val His
162 625          630
163 CATGCCTCAG GCTTCTGCAG CCCAGGGCAC TAAAACGTCT CACACTCAGA GCCGGCTGGC      1982
164 CCGGGAGCTC CTTGCCTGCC ATTTTCTCCA GGGGACAGAA TAACCCAGTG GAGGATGCCA      2042
165 GGCTGGAGA CGTCCAGCCG CAGGCGGCTG CTGGGCCCCA GGTGGCGCAC GGATGGTGAG      2102
166 GGGCTGAGAA TGAGGGCACC GACTGTGAAG CTGGGGCATC GATGACCCAA GACTTTATTT      2162
167 TTTGAAAAAT ATTTTTCAGA CTCCTCAAAC TTGACTAAAT GCAGCGATGC TCCCAGCCCA      2222
168 AGAGCCCATG GGTCGGGGAG TGGGTTTGA TAGGAGAGCT GGGATTCCAT CTCGACCCTG      2282
169 GGGCTGAGGC CTGAGTCCTT TTGGATTCTT GGTACCCACA TTGCCTCCTT CCCCTCCTTT      2342
170 TTTCAGGGGT GGGTGGTTGG TGTTCCTGAA GACCCAGGGA TACCCTTTGT CCAGCCCTGT      2402
171 CCTTGGCAGC TCCCTTTTTG GTCCTGGGTC CCACAGGACA GCCGCCTTGC ATGTTTATTG      2462
172 AAGGATGTTT GCTTTCGGA CGGAAGGACG GAAAAA      2498
173
174 (2) INFORMATION FOR SEQ ID NO:2:
175 (i) SEQUENCE CHARACTERISTICS:
176 (A) LENGTH: 634 amino acids
177 (B) TYPE: amino acid
178 (D) TOPOLOGY: linear
179 (ii) MOLECULE TYPE: protein
180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
181 Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu
182 1 5 10 15
183 Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln
184 20 25 30
185 Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His
186 35 40 45
187 Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr
188 50 55 60
189 Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn
190 65 70 75 80
191 Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn
192 85 90 95
193 Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly
194 100 105 110
195 Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val
196 115 120 125
197 Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu
198 130 135 140
199 Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg
200 145 150 155 160
201 Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly
202 165 170 175
203 Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe
204 180 185 190
205 Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/041,236

DATE: 12/03/98  
TIME: 13:51:26

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206		195		200		205	
207	Tyr	Tyr	Phe	Phe	Arg	Glu	Asp
208		210				215	
209	Leu	Asn	Val	Ser	Arg	Val	Ala
210	225				230		
211	Glu	Ser	Ser	Leu	Ser	Val	Ser
212					245		
213	Leu	Val	Cys	Ser	Asp	Ala	Ala
214					260		
215	Asp	Val	Phe	Leu	Leu	Pro	Asp
216		275				280	
217	Val	Tyr	Gly	Val	Phe	Ser	Asn
218		290				295	
219	Tyr	Ser	Leu	Gly	Asp	Ile	Asp
220	305					310	
221	Gly	Tyr	His	Ser	Ser	Leu	Pro
222					325		
223	Asp	Gln	Gln	Pro	Ile	Pro	Thr
224					340		
225	Pro	Glu	Val	Ala	Gln	Arg	Val
226		355				360	
227	Leu	Phe	His	Ser	Lys	Tyr	His
228		370				375	
229	Gln	Ala	Ser	His	Gly	Glu	Thr
230	385					390	
231	Arg	Gly	Thr	Ile	His	Lys	Val
232					405		
233	Phe	Ala	Phe	Asn	Ile	Met	Glu
234					420		
235	Ile	Gln	Thr	Met	Ser	Leu	Asp
236		435				440	
237	Ser	Gln	Trp	Glu	Val	Ser	Gln
238		450				455	
239	Gly	Gly	Gly	Cys	His	Gly	Cys
240	465					470	
241	Trp	Asp	Gln	Gly	Arg	Cys	Ile
242					485		
243	Leu	Gln	Ser	Ile	Asn	Pro	Ala
244					500		
245	Lys	Pro	Asp	Lys	Ala	Pro	Leu
246		515				520	
247	Arg	Tyr	Tyr	Leu	Ser	Cys	Pro
248		530				535	
249	Trp	Arg	His	Lys	Glu	Asn	Val
250	545					550	
251	Ser	Pro	Asn	Cys	Ile	Leu	Phe
252					565		
253	Gly	His	Tyr	Phe	Cys	Glu	Ala
254					580		
255	Gln	His	Trp	Gln	Leu	Leu	Pro
256		595				600	
257	Leu	Gly	His	Ala	Cys	Ala	Leu
258		610				615	

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/041,236**

DATE: 12/03/98  
TIME: 13:51:27

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Original Text